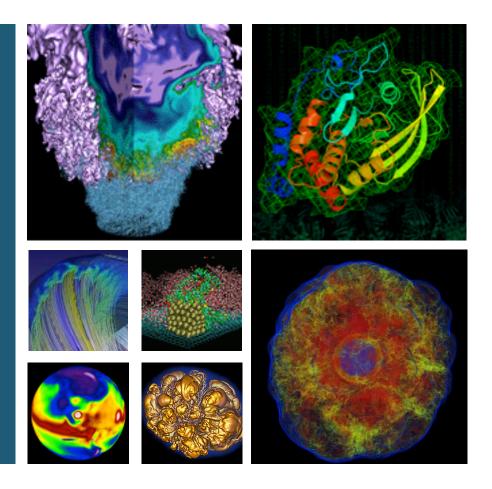
Workflow Tools at NERSC







NERSC User Meeting March 21st, 2016



What Does Workflow Software Do?



Automate connection of applications

- Chain together different steps in a job pipeline.
- Automate provenance tracking -> enable ability to reproduce results.
- Assist with data movement.
- Monitor running processes and handle errors.
- Data processing of streaming experimental data (including near-realtime processing).
- Workflows help work with (around?) batch scheduler and queue policies.





Workflows are Personal



- Many tools exist in the workflow space
 - Google: "Scientific Workflow Software"
- It seems like each domain has its own workflow solution to handle domain-specific quirks
- No single tool solves every single problem
 - Fireworks
 - qdo
 - Tigres
 - Galaxy
 - Swift

- BigPanda
- Pegasus
- Taverna
- Airavata
- •





Workflows Working Group



- Last year Workflows working group investigated breadth of technologies
- We 'support' 2 tools at NERSC
 - -FireWorks
 - -Swift
 - -this doesn't mean other tools won't be used/supported at NERSC, only that DAS has specific expertise in these.
- Create an ecosystem to enable self-supported WF tools
 - Databases, User defined software modules, AMQP services etc.





Existing Workflow Ecosystem @ NERSC



- Science Gateways
- Databases
 - Mongo, Postgres, MySQL, SQLite, SciDB
- Workflow tools (self-supported)
 - Fireworks, swift, Tigres, qdo, Galaxy
- High throughput batch queues
- NEWT REST API
- Globus / Data Transfer Nodes
- Many task frameworks
 - MySGE, Taskfarmer
- Other web based tools for interactive use cases
 - iPython, R Studio, NX
- MapReduce frameworks
 - Spark, Hadoop

Workflow tools
exist in and
interact with a rich
environment of
NERSC capabilities
and services.

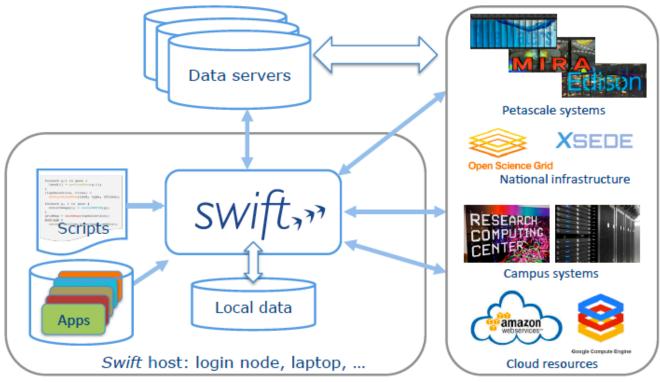




Use Case: Swift



- Enables execution over multiple compute resources
- Swift language "encapsulates" application, easing distribution, parallelisation and provenance capture









Use Case: Swift (Biosciences)

- Functional language: powerful parallel loops
- Example: protein simulation for drug screening

```
Sweep(Protein pSet[])
                                                     O(10) proteins
 int nSim = 1000;
                                                     implicated in a disease
 int maxRounds = 3;
 float startTemp[] = [100.0, 200.0];
 float delT[] = [1.0, 1.5, 2.0, 5.0, 10.0];
 foreach p, pn in pSet {
   foreach t in startTemp {
     foreach d in delT {
      IterativeFixing(p, nSim, maxRounds, t, d);
                   10 proteins x 1000 simulations x
                    3 rounds x 2 temps x 5 deltas
                              = 300K tasks
```





Workflows and Data Intensive Science



- Data intensive scientific computing may not always fit the traditional HPC paradigm
 - Large numbers of tasks, low degree of parallelism.
 - Job dependencies and chaining.
 - Need to communicate with external datasources, DBs.
- Workflow and work orchestration in this context can be thought of as sequences of compute and data-centric operations.





High Throughput "Bag of Tasks"



- Often need to process large numbers of smallish tasks repeatedly.
- Typical queue policies work against you
 - a lot of time lost waiting.
 - Batch system not set up for lots of little tasks.
- Instead use a workflow system
 - to queue up tasks.
 - to launch long running workers to consume these tasks.

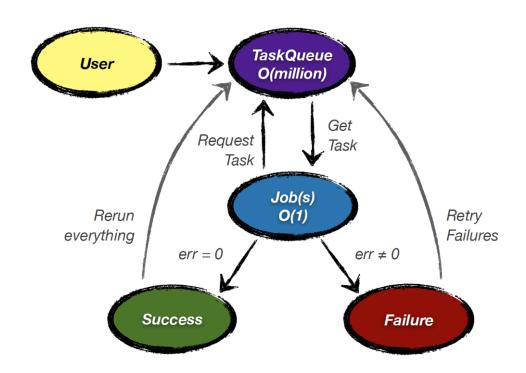








qdo Model



 qdo is specifically designed to package up multiple small tasks into one batch job.





qdo examples



```
#- Command line
qdo load Blat commands.txt #- loads file with commands
qdo launch Blat 24 --pack #- 1 batch job; 24 mpi workers
#- Python
import qdo
q = qdo.create("Blat")
for i in range(1000):
   q.add("analyze blat{}.dat".format(i))
q.launch(24, pack=True)
#- Python load 1M tasks
commands = list()
for x in range(1000):
    for y in range (1000):
        commands.append("analyze -x \{\} -y \{\}".format(x, y))
q.add_multiple(commands) #- takes ~2 minutes
q.launch(1024, pack=True)
```





Many-task frameworks



- Repeatedly perform tasks on a large dataset
- Map => perform an operation across a large set i.e. map a task across the dataset
- Reduce => collect and reduce the results from map operation
- Split the data across nodes and run task on each node
- Typically does not require much cross node communication
- Frameworks at NERSC
 - Spark
 - Hadoop

- MySGE
- Taskfarmer





Batch Queues



- NERSC has queues suited to jobs that need less than one compute core
 - -Cori Shared queue designed specifically for these use cases.
- Reservations available for special needs.
- Consider using job packing options in various workflow tools to optimize for HPC queue infrastructure
 - –also for packing single-core jobs into a multi-core node.





Use Case: TaskFarmer



- Simple NERSC-developed utility that farms single-core tasks onto a multi-core compute node, tracks job success
- 1) Write a wrapper that defines one task to run

cd \$SCRATCH/myDir
python myScript.py \$1 \$2 \$3

2) Make list of tasks to run, with options to pass to your wrapper

wrapper.sh 0 0 1 wrapper.sh 0 1 0 wrapper.sh 0 1 1

3) Write a batch script that will run your tasks on compute nodes

http://www.nersc.gov/users/data-analytics/workflow-tools/taskfarmer

#SBATCH -N 2 -c 32

#SBATCH -p debug

#SBATCH -t 00:05:00

cd \$SCRATCH/myDir

export THREADS=32

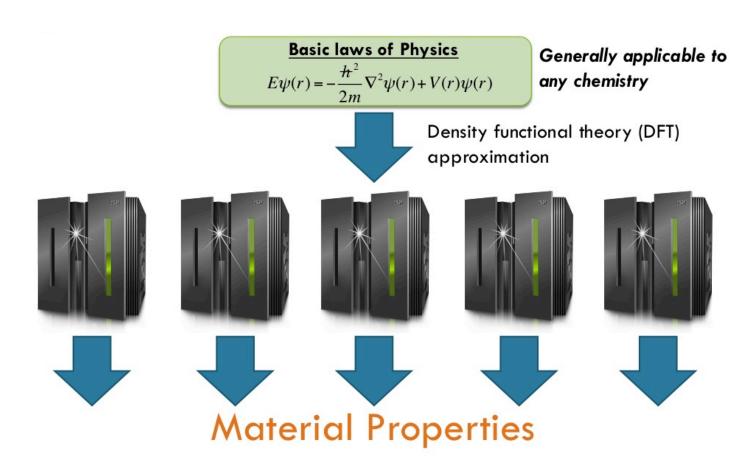
runcommands.sh tasks.txt

#!/bin/sh



Putting it all together: Materials Project VEARS of the street of the st

Simulate properties of all possible materials.

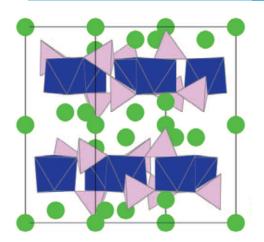




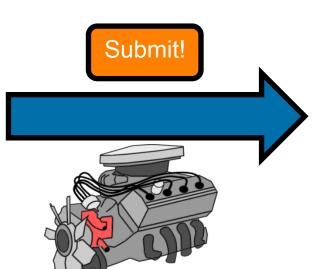


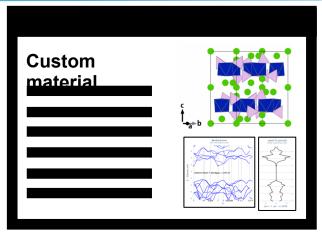


Materials Project Workflow



input: A cool material!!





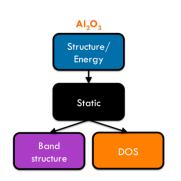
output: Lots of information about cool material!!



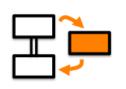




Input generation (parameter choice)











Workflow mapping

Office of Science

Supercomputer submission / monitoring

Error handling

File Transfer

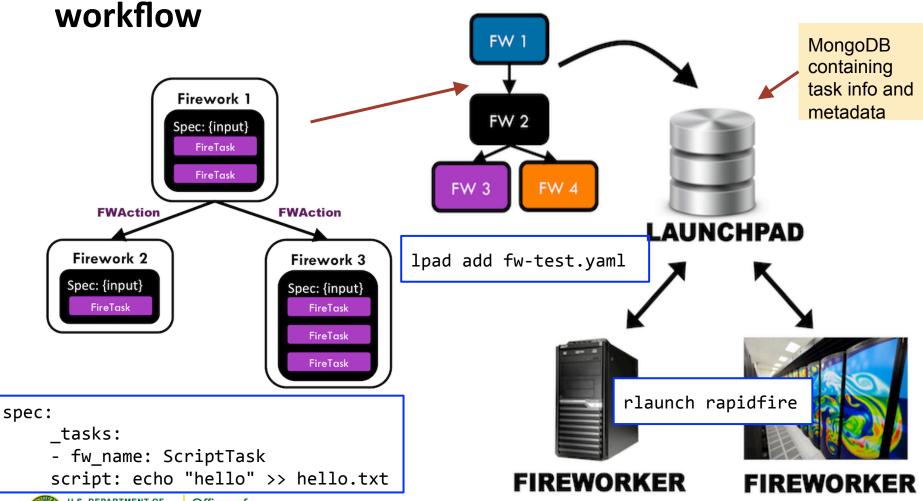
File Parsing / DB insertion



Use Case: Materials Project



Fireworks used to organise simulation and data







NERSC YEARS at the FOREFRONT

Use Case: Materials Project

- Tasks submitted to Fireworks MongoDB via API/ python script etc.
- MongoDB keeps track of all tasks
- Fireworks submits workers to NERSC queues.
- Workers pull jobs from MongoDB.
- Fireworks manages job orchestration
 - Retry on failure
 - File transfer
 - Job Dependencies
 - Flow control for subsequent jobs
 - Duplicate management





Fireworks: Error Handling and Dynamic Workflows



- Can change next step of workflow, based on outcome of previous step
- Can specify action based on soft failures, hard failures, human errors
 - "lpad rerun –s FIZZLED"
 - "lpad detect_lostruns –rerun"

"dead" job

main thread

ping_thread







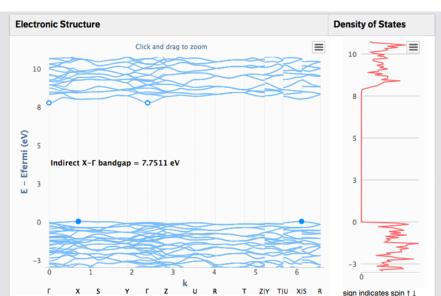


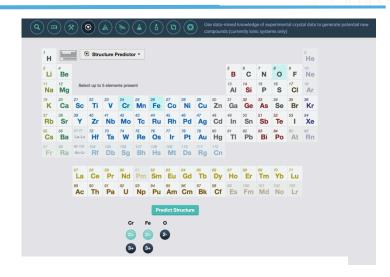


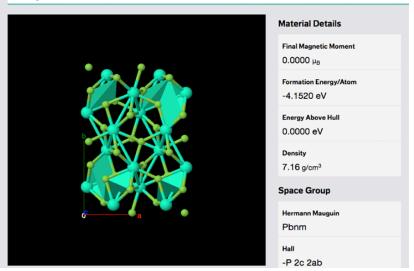
Materials Project Gateway















MATERIAL

TbF₃

Finding the Right Hammer





- Workflow tools have lots of features but there is no one size-fits-all
- NERSC is building expertise in classes of workflow tools and will help guide you towards the right tool for your job
- Consider stitching together a couple of different tools to make it all work for you.





Thank you.



